

Article ID:1005-3085(2010)06-1105-06

HIV-1 Transmission Dynamics Among Injecting Drug Users on a Risk Network Model*

LOU Jie, CHEN Li

(Department of Mathematics, Shanghai University, Shanghai 200444)

Abstract: Using a “risk network” to describe the contact patterns (including needle sharing and sex behavior) of buddy relationships in injecting drug users (IDUs), a stochastic model is studied about the spreading of HIV-1 in IDUs. The basic reproduction number and the final size of the epidemic are obtained. In particular, the model has been applied to Xichang city. Through simulations, the effect of the injecting network size (and also the sex network size) in the spreading of HIV-1 in IDUs are studied. The model shows that 10% increasing of the final size of the epidemic need only one triple of needle sharing added for one IDU. The results give us very important hint: reduce the network sizes, especially the needle sharing network size should be a very important intervention measure to control the spread of HIV-1 in IDUs.

Keywords: HIV/AIDS; risk network; basic reproduction number; IDUs

Classification: AMS(2000) 34C25; 34D23 **CLC number:** O175.7 **Document code:** A

1 Introduction

HIV-1 is an infectious pathogen that is now largely spread through close personal contact. A “risk network” is comprised of those people among whom HIV-1 risk behaviors occur. Risk networks thus act as conduits of infection. The role of risk networks as conduits of HIV-1 infection is illustrated by studies^[1-3] that have focused on IDUs in Sichuan province and Xinjiang province, China. Qualitative data were collected and were used to construct sociograms of the risk networks of drug injectors. Authors found that the size of risk network of sharing injection equipment among IDUs has positive association with HIV-1 infection. We use the term “risk network” to describe the contact patterns (including needle sharing and sex behavior) of buddy relationships that are stable over a longer time. So the problem here is how to find a graph that captures the social formations in drug users in a satisfactory way.

IDUs in China normally have two risk social relationships which are suited for the spread of HIV-1: one is the “buddy relationship” (needle sharing network), and each group size is not very big (normally include about 2 to 3 people). The other is the “sexual relationships”. We will use an undirected graph to describe the spread of the epidemic. Given a set of N labeled vertices. The risk network will be constructed in the following way:

Received: 17 Dec 2008.

Biography: Lou Jie (Born in 1973), Female, Ph.D.

Accepted: 24 Feb 2010.

Research field: mathematical biology.

***Foundation item:** The National Natural Science Foundation of China (10701053; 11072136); the Shanghai Leading Academic Discipline Project (S30104); the International Development Research Center of Canada (104519-010).

- 1) We add edges in all vertices (v_i, v_j) with probability r_d , and the subgraph that is generated is denoted by G^d ;
- 2) We add edges in all possible triples of vertices (v_i, v_j, v_k) , $i, j, k = 1, \dots, N$, $i \neq j \neq k$ (call them triangles) with probability \tilde{r}_d , and the subgraph that is generated is denoted by \tilde{G}^d ; Both G^d and \tilde{G}^d represent the needle sharing network;
- 3) We add edges randomly in all vertices (v_i, v_j) , $i, j = 1, \dots, N$, $i \neq j$ with probability r_s , and the subgraph that is generated is denoted by G^s . Let it represent the "sexual relationship" structure.

So this construction procedure generates a graph G that can be written as the union of three independent subgraphs G^d , \tilde{G}^d and G^s . Also, we call r_s , \tilde{r}_d and r_d as network probabilities.

Given a graph G generated as above. The average coordination number z for a given vertex v in G is

$$z = \sum_{i=s,d} r_i(N-1) + 2\tilde{r}_d C_2^{(N-1)}.$$

Since no people can have infinite friends, we put

$$r_i = \lambda_i / (N-1), \quad i = s, d, \quad \tilde{r}_d = \tilde{\lambda}_d / (C_2^{(N-1)})$$

for some $\lambda_i > 0$ ($i = s, d$) and $\tilde{\lambda}_d > 0$ to scale the edge probability in G . Here λ_d , λ_s and $\tilde{\lambda}_d$ are the average numbers of two-people fellowship of needle sharing, sexual fellowship and triangle fellowship of needle sharing of vertex v respectively.

In the following we discuss what will happen if we let HIV spread along graph G . We consider a closed population, consisting of N individuals. Let n denote the initial number of susceptible individuals and m (which is very small compare with n) be the initial number of infectious individuals. All individuals in the network are labeled as either susceptible (S), infected (I) or removed (R).

2 The basic reproduction number and the final size of the epidemic

First we assume that addicts sequentially use the same drug-injection equipment in \tilde{G}^d . Any uninfected addict who uses infectious injection equipment is considered to be exposed to HIV-1 of course a given HIV-1 infective can only infect his buddies (e.g., his sex partners by probability p_s or his drug injecting partners by probability \tilde{p}_d and p_d). Also the infection probabilities should be thought of as a product of the contact probability and the probability of a disease transmission in case of a contact, thus giving the probability of a contact resulting in a new infective.

Now provided that the population is large, contacted individuals in the epidemic process are susceptible with high probability in the beginning of the time course. Thus the initial stage in the generation process of infective is well approximated by a branching process with reproduction mean equal to the average number of new cases generated by a given infective. We denote it as the basic reproduction number R_0 . This is a critical parameter indicating whether or not a large outbreak is possible. If $R_0 \leq 1$ then the asymptotic probability of a large outbreak is zero, while if $R_0 > 1$, then there is, asymptotically, a strictly positive probability of a large

outbreak. By a large outbreak we mean an outbreak such that the size of the outbreak is of the same order as the whole population.

For $G = G^s \cup \tilde{G}^d \cup G^d$. Let R_s , \tilde{R}_d and R_d denote the expected numbers of secondary cases generated by an infected individual i in G^s , \tilde{G}^d and G^d respectively. Then $R_0 = R_s + \tilde{R}_d + R_d$.

Let X^s and X^d denote the degree of vertex i in G^s and G^d , respectively, and \tilde{X}^d is the number of triangles in \tilde{G}^d involving vertex i .

Since each of these individuals is infected by i with probability p_s in G_1 for sex active people, hence $R_s = p_s E[X^s] = p_s \lambda_s$. Similar can get that $R_d = p_d E[X^d] = p_d \lambda_d$.

About \tilde{R}_d , it should be the product of two expectations: one expectation is of the number of triangles in \tilde{G}^d involving i , that is, $E[\tilde{X}^d] = \tilde{\lambda}_d$; the other expectation is of the number of secondary cases generated by i in a fixed triangle, we denote it as $E[\tilde{Y}^d]$. All the possible values of \tilde{Y}^d should be 0, 1 or 2. It is easy to get that the probability of only one new infective is $2\tilde{p}_d(1 - \tilde{p}_d)^2$ since \tilde{p}_d is the transfer probability by the 3-clique sharing injecting equipment group. In case of two new infectives, there are two possibilities: the two new infectives are infected directly by i , which probability is \tilde{p}_d^2 ; or the infection takes place in two steps, which probability is $2(1 - \tilde{p}_d)\tilde{p}_d^2$. So

$$E[\tilde{Y}^d] = 2\tilde{p}_d(1 - \tilde{p}_d)^2 + 2[\tilde{p}_d^2 + 2(1 - \tilde{p}_d)\tilde{p}_d^2], \quad \tilde{R}_d = E[\tilde{X}^d]E[\tilde{Y}^d] = 2\tilde{\lambda}_d(\tilde{p}_d + \tilde{p}_d^2 - \tilde{p}_d^3).$$

Let R^d be the total reproduction number of sharing injecting equipment groups including these 2-cliques and these 3-cliques, that is $R^d = \tilde{R}_d + R_d$, then we have

$$R_0 = R_s + R^d = \lambda_s p_s + 2\tilde{\lambda}_d(\tilde{p}_d + \tilde{p}_d^2 - \tilde{p}_d^3) + \lambda_d p_d.$$

In the following, we study the final size of the epidemic. Suppose the initial infected individuals number N_0 is very small. Define τ_s , $\tilde{\tau}_d$ and τ_d as the proportion of the initially susceptible individuals in G^s , \tilde{G}^d and G^d , respectively, that is ultimately infected. Define τ as the proportion of the whole initially susceptible individuals that is ultimately infected. Asymptotically the probability that a given individual is infected should equal to the proportion of the population that is ultimately infected in the epidemic.

Now consider a given susceptible individual i . Let A denote the event that i is infected. Let B , C and D denote the event that i is infected through G^s , \tilde{G}^d , or G^d , respectively. Then

$$\begin{aligned} P(\bar{A}) &= P(\bar{B})P(\bar{C})P(\bar{D}), \quad \tau_s = P(B), \quad \tilde{\tau}_d = P(C), \quad \tau_d = P(D), \\ \tau &= \tau_s + \tilde{\tau}_d + \tau_d - \tau_s \tilde{\tau}_d - \tau_s \tau_d - \tilde{\tau}_d \tau_d + \tau_s \tilde{\tau}_d \tau_d. \end{aligned} \quad (1)$$

Let B_j denote the event that i is infected from a given neighbor j in G^s . Then

$$P(B_j) = \tau_s p_s + (1 - \tau_s)0 = \tau_s p_s, \quad P(\bar{B}) = E[P(\bar{B}_j)^{X^s}] = E[(1 - \tau_s p_s)^{X^s}].$$

Take the right-hand side in the above equality as the probability generating function of X^s evaluated at $1 - \tau_s p_s$, then $\tau_s = 1 - e^{-\tau_s p_s \lambda_s}$. Using similar way we can get that $\tau_d = 1 - e^{-\tau_d p_d \lambda_d}$.

Now we consider $P(\bar{C})$. Since we suppose that the number of triangles in \tilde{G}^d involving vertex i is \tilde{X}^d , so

$$P(\bar{C}) = E\left[P\left(\bar{C}_1 \cap \bar{C}_2 \cap \cdots \cap \bar{C}_{\tilde{X}^d}\right)\right] = E[P(\bar{C}_V)^{\tilde{X}^d}], \quad V = 1, 2, \dots, \tilde{X}^d, \quad (2)$$

where \bar{C}_V means that i escapes infection in a fix triangle $V = \{i, j, k\}$.

Let Λ denote the event that j and k will be both infected as soon as one of them is infected. Then

$$P(\bar{C}_V) = P(\bar{C}_V | \Lambda)P(\Lambda) + P(\bar{C}_V | \Lambda^c)P(\Lambda^c). \quad (3)$$

Now we have three possible situations: both k and j are not infected; one of j and k is infected; and both k and j are infected. According to our definition of $\tilde{\tau}_d$, the asymptotic probability for an individual to escape infection is equal to $1 - \tilde{\tau}_d$. So from (3) we can get

$$\begin{aligned} P(\bar{C}_V) &= \tilde{p}_d[(1 - \tilde{\tau}_d)^2 + 2\tilde{\tau}_d(1 - \tilde{\tau}_d)(1 - \tilde{p}_d)^2 + \tilde{\tau}_d^2(1 - \tilde{p}_d)^2] \\ &\quad + (1 - \tilde{p}_d)[(1 - \tilde{\tau}_d)^2 + 2\tilde{\tau}_d(1 - \tilde{\tau}_d)(1 - \tilde{p}_d) + \tilde{\tau}_d^2(1 - \tilde{p}_d)^2] \\ &= 1 - [2\tilde{p}_d\tilde{\tau}_d(2 - \tilde{\tau}_d) + \tilde{p}_d^2\tilde{\tau}_d(2 - 3\tilde{\tau}_d) - 2\tilde{p}_d^3\tilde{\tau}_d(1 - \tilde{\tau}_d)]. \end{aligned}$$

Looking at the right-hand side in equality (2) as the probability generating function of \tilde{X}^d evaluated at $P(\bar{C}_V)$, also \tilde{X}^d is asymptotically Poisson ($\tilde{\lambda}_d$) distributed, then

$$P(\bar{C}) = e^{-\tilde{\lambda}_d[2\tilde{p}_d\tilde{\tau}_d(2 - \tilde{\tau}_d) + \tilde{p}_d^2\tilde{\tau}_d(2 - 3\tilde{\tau}_d) - 2\tilde{p}_d^3\tilde{\tau}_d(1 - \tilde{\tau}_d)]}.$$

So

$$\tilde{\tau}_d = 1 - e^{-\tilde{\lambda}_d[2\tilde{p}_d\tilde{\tau}_d(2 - \tilde{\tau}_d) + \tilde{p}_d^2\tilde{\tau}_d(2 - 3\tilde{\tau}_d) - 2\tilde{p}_d^3\tilde{\tau}_d(1 - \tilde{\tau}_d)]}$$

and equation (1) holds too, that is

$$\tau = \tau_s + \tilde{\tau}_d + \tau_d - \tau_s\tilde{\tau}_d - \tau_s\tau_d - \tilde{\tau}_d\tau_d + \tau_s\tilde{\tau}_d\tau_d.$$

3 Applying to Xichang city

To get the infection probabilities p_s , \tilde{p}_d and p_d , we define

$$p_s = h_s n_s (1 - e_s c_s), \quad \tilde{p}_d = h_d \tilde{n}_d (1 - e_d c_d), \quad p_d = h_d n_d (1 - e_d c_d),$$

in which, h_s is the transmissibility by sex connection, and n_s is the sexual frequency between the infected individual and one of his sex partner. The transmission of HIV-1 also depends on condom efficacy, e_s , and the frequency of condom use, c_s , between the infected individual and his sex partners. We use h_d represent the transmissibility that an addict becomes infected given exposure to HIV-1. It is the infectivity of HIV-1 via shared injection equipment. \tilde{n}_d and n_d denote the sharing frequency of injection equipment between the infected individual and one of his friends in \tilde{G}^d and G^d respectively. Also we assume that an addict cleans the needle with probability c_d prior to use, and parameter e_d means the efficacy of the cleaning. According to literatures^[1-6], we choose the following parameters values as that in Figure 1 and Figure 2 for a given vertex v in G .

First we discuss how the injecting network size (and also the sex network size) effect the outcomes of HIV spreading. Let λ_s , λ_d and $\tilde{\lambda}_d$ denote the sizes of the sex network and the injecting network. The relationship between the reproduction number R_0 and the sex network

size λ_s can be seen in Figure 1. This figure shows clearly that the reproduction numbers R_s and R_0 increase quite fast along with the increasing of the sex network's dimension. The star points are the reproduction numbers of the parameters in Figure 1 and $\lambda_s = 3$. Similar trend curves can be got for the relationship between the reproduction number R_0 and the needle sharing network size of IDUs, $\tilde{\lambda}_d$.

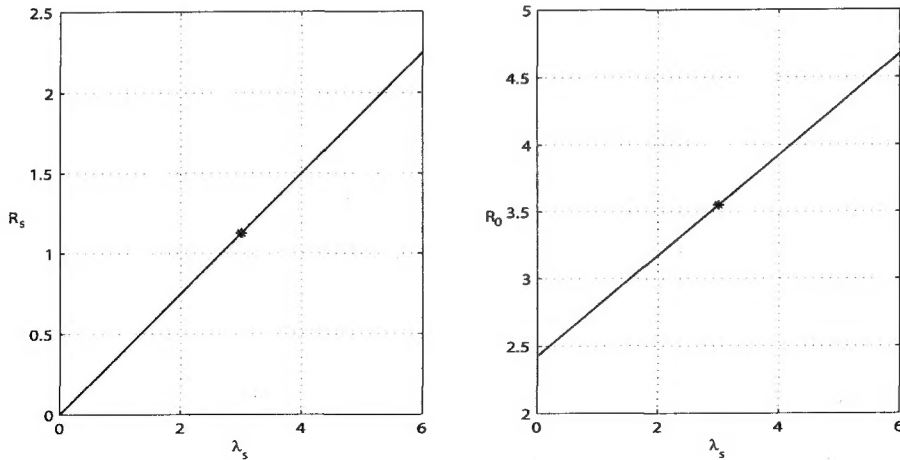


Figure 1: R_s and R_0 increase fast along with the increasing of the sex network size λ_s . Other parameters are chosen as $\tilde{\lambda}_d = 2$, $\lambda_d = 3$, $h_s = 0.05$, $h_d = 0.3$, $n_s = 8$, $e_s = 0.7$, $c_s = 0.09$, $n_d = 1.3395$, $\tilde{n}_d = 0.893$, $c_d = 0.04$, $e_d = 0.6$.

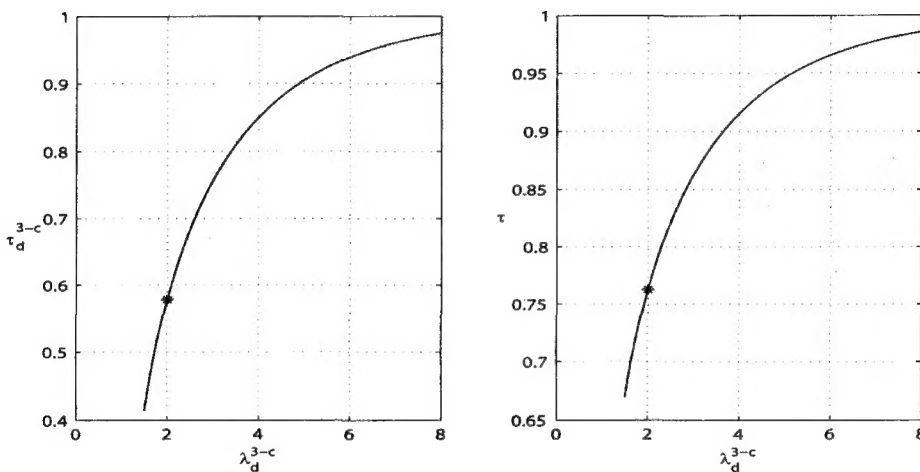


Figure 2: $\tilde{\tau}_d$ and τ increase very fast along with the increasing of the risk network size $\tilde{\lambda}_d$ (i.e., λ_d^{3-c}). Other parameters are chosen as $\lambda_s = 3$, $\lambda_d = 3$, $h_s = 0.05$, $h_d = 0.3$, $n_s = 8$, $e_s = 0.7$, $c_s = 0.09$, $n_d = 1.3395$, $\tilde{n}_d = 0.893$, $c_d = 0.04$, $e_d = 0.6$.

The importance of the size of the risk network in the spreading of HIV-1 in IDUs, especially for the number of sex partners and the needle sharing triple, can be seen from simulations. The size of needle sharing network (which includes these triples) contributes much more to the spreading of HIV-1 in IDUs than that of the sexual network. Figure 2 shows that, 10% increasing of the final size of the epidemic need only one triple of needle sharing added for one IDU.

So we conclude that, reduce both of the network sizes, especially the needle sharing network size should be a very important method to control the spread of HIV-1 in IDUs in China.

References:

- [1] Ma M, Chen Xi, *et al.* Study on the relationship between HIV infection and pattern of sharing injection equipment among intravenous drug users[J]. J Prev Med Inf, 2005, 21: 647-650
- [2] Li X X, *et al.* HIV-1 prevalence and associated risk factors among injection drug users in Xichang county of Sichuan province[J]. China J Mat Med, 2006, 8: 161-164
- [3] Qin G, Yang Ye, *et al.* Study on mode of HIV-1 infection among drug users in Xichang county of Sichuan province[J]. Modern Preventive Medicine, 2006, 133: 354-357
- [4] Longini J M, Clark W, Haber M, *et al.* The stages of HIV-1 infection: waiting times and infection transmission probabilities[C]// Mathematical and Statistical Approaches to AIDS Epidemiology, Lecture Notes in Biomathematics Vol 83, Berlin: Springer Verlag, 1989: 111-137
- [5] Jacquez J A, Koopman J S, Simon C P, *et al.* Role of the primary infection in epidemics of HIV-1 infection in gay cohorts[J]. J Acquir Immune Defic Syndr, 1994, 7: 1169-1184
- [6] Gray R H, Wawer M J, Brookmeyer R, *et al.* Probability of HIV-1-1 transmission per coital act in monogamous, heterosexual, HIV-1-1-discordant couples in Rakai, Uganda[J]. Lancet, 2001, 357: 1149-1153

基于危险网络上的吸毒人群中 HIV 的传播

姜 洁, 陈 立

(上海大学理学院数学系, 上海 200444)

摘 要: 通过建立吸毒人群中交往关系(包括针具共用和性关系)的“危险关系网络”, 我们研究了一个关于 HIV 在此人群中传播的随机模型, 得到了基本再生数和最终感染者比例。使用四川省西昌市的调查数据, 我们研究了针具共用以及性关系的网络规模对模型最终结果的影响。模拟发现, 每个注射吸毒者每增加一个“三人小圈子”网络, 将最终导致增加 10% 的感染者。结果提示: 减少危险关系网络的规模, 尤其是针具共用的网络规模, 对控制 HIV 的传播有重要的作用。

关键词: HIV/AIDS; 危险网络; 基本再生数; IDUs